AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Claim 1 (currently amended): An isolated compound which inhibits pilus assembly**, or a pharmaceutically-acceptable salt thereof**, said compound comprising a mimic of a chaperone G1 beta-strand or a mimic of an amino terminal motif of a pilus subunit, wherein the mimic is a 10 to 20 residue peptide, having an amino terminus and a carboxy terminus, according to formula (I):

~~(I)~~ Z_1~Z_2–X_1–X_2–X_3–X_4–X_5–X_6–X_7–X_8–X_9–X_{10}–Z_3~Z_4 **(I)** ~~or a pharmaceutically-acceptable salt thereof,~~

wherein:

Z_1 is the amino terminus of the mimic peptide, Z_1 having the formula R-C(O)-NR- or RRN-;

Z_2 is (i) a first peptide sequence consisting of 1 to 5 amino acid residues or (ii) a bond connecting Z_1 to X_1;

X_1 is any amino acid residue;

X_2 is any amino acid residue;

X_3 is a hydrophobic residue or a hydroxyl-substituted aliphatic residue;

X_4 is any amino acid residue;

X_5 is a hydrophobic residue or Gly;

X_6 is a hydrophobic or a hydrophilic residue;

X_7 is Gly, an amide-substituted polar residue or a hydrophobic residue;

X_8 is an amino acid residue other than an aliphatic residue;

X_9 is an aliphatic residue;

X_{10} is any amino acid residue;

Z_3 is (i) a second peptide sequence consisting of 1 to 5 amino acid residues or (ii) a bond connecting Z_4 to X_{10};

Z_4 is the carboxy terminus of the peptide, Z4 having the formula –C(O)OR or –C(O)NRR;

each R is independently hydrogen, (C_1-C_6) alkyl, (C_2-C_6) alkenyl, (C_2-C_6) alkynyl or (C_6-C_{14}) aryl;

each "–" between residues X_1 through X_{10}, Z_2 and X_1 and X_{10} and Z_3 independently represents an amide linkage, a substituted amide linkage or an isostere of an amide linkage; and

each "~" represents a bond.

Claim 2-3 (cancelled)

Claim 4 (previously presented): The compound of claim 1 wherein the compound exhibits antibacterial activity against a Gram-negative bacterium.

Claim 5 (currently amended): **An isolated compound which inhibits pilus assembly, said compound comprising SEQ ID NO: 1, wherein the compound is a mimic of a chaperone G_1 beta-strand and the compound exhibits antibacterial activity against a Gram-negative bacterium.** ~~**The compound of claim 4 wherein said mimic comprises SEQ ID NO: 1 or an analog thereof.**~~

Claim 6 (cancelled)

Claim 7 (cancelled)

Claim 8 (previously presented): The compound of claim 1 wherein the compound comprises a mimic of an amino terminal motif of a pilus subunit selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO:

22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28 and SEQ ID NO: 29.

Claim 9 (currently amended): The compound of claim 8 wherein said mimic of an amino-terminal motif of a pilus subunit further comprises the amino acid sequence SDVAFRGNLL (SEQ ID NO: 12) ~~or an analog thereof~~.

Claim 10 (cancelled)

Claim 11 (cancelled)

Claim 12 (cancelled)

Claim 13 (previously presented): The compound of claim 1 wherein one or more of the following conditions are satisfied:

each "–" between residues X_1 through X_{10}, Z_2 and X_1 and X_{10} and Z_3 is an amide linkage;

Z_1 is H_2N–;

Z_4 is –C(O)OH or a salt thereof;

Z_2 is a bond connecting Z_1 to X_1;

Z_3 is a bond connecting Z_4 to X_{10};

X_1 is an amino acid residue other than a basic residue;

X_2 is an amino acid residue other than an aliphatic residue;

X_3 is an aliphatic residue or T;

X_4 is an amino acid residue other than an acidic residue;

X_5 is an aliphatic residue, F or G;

X_7 is G, N or A; or

X_{10} is an aliphatic or a polar residue.

Claim 14 (previously presented): The compound of claim 13 wherein the mimic comprises a sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID

NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28 and SEQ ID NO: 29.

Claim 15 (cancelled)

Claim 16 (currently amended): An isolated compound which inhibits pilus assembly**, or a pharmaceutically-acceptable salt thereof**, the compound comprising a mimic of a chaperone G_1 beta-strand or a mimic of an amino terminal motif of a pilus subunit, wherein the mimic is a 7 to 17 residue peptide ~~or peptide analog~~, having an amino terminus and a carboxy terminus, according to formula (II):

~~(II)~~ Z_{11} ~Z_{12}–X_{11}–X_{12}–X_{13}–X_{14}–X_{15}–X_{16}–X_{17}–Z_{13}~ Z_{14} **(II)**

~~or a pharmaceutically-acceptable salt thereof,~~

wherein:

Z_{11} is the amino terminus of the peptide, Z_{11} having the formula R'–C(O)–NR'– or R'R'N–;

Z_{12} is (i) a first peptide sequence consisting of 1 to 5 amino acid residues or (ii) a bond connecting Z_{11} to X_{11};

X_{11} is any amino acid residue;

X_{12} is any amino acid residue;

X_{13} is a hydrophobic residue;

X_{14} is any amino acid residue;

X_{15} is a hydrophobic residue;

X_{16} is any amino acid residue;

X_{17} is hydrophobic residue or a hydroxyl-substituted aliphatic residue;

Z_{13} is (i) a second peptide sequence consisting of 1 to 5 amino acid residues or (ii) a bond connecting Z_{14} to X_{17};

Z_{14} is the carboxy terminus of the peptide, Z_{14} having the formula –C(O)OR' or –C(O)NR'R';

each R' is independently hydrogen, (C_1-C_6) alkyl, (C_2-C_6) alkenyl, (C_2-C_6) alkynyl or (C_6-C_{14}) aryl;

each "–" between residues X_{11} through X_{17}, Z_{12} and X_{11} and X_{17} and Z_{13} independently represents an amide linkage, a substituted amide linkage or an isostere of an amide linkage; and

each "~" independently represents a bond.

Claim 17 (previously presented): The compound of claim 16 wherein one or more of the following conditions are satisfied:

each "–" between residues X_{11} through X_{17}, Z_{12} and X_{11} and X_{17} and Z_{13} is an amide linkage;

Z_{11} is H_2N–;

Z_{14} is –C(O)OH or a salt thereof;

Z_{12} is a bond connecting Z_{11} to X_{11};

Z_{13} is a bond connecting Z_{14} to X_{17};

X_{11} is an amino acid residue other than a basic residue;

X_{13} is an aliphatic residue or M;

X_{14} is an amino acid residue other than an aromatic residue;

X_{15} is an aliphatic residue, F or M; and

X_{17} is an aliphatic residue, F, M or a hydroxyl-substituted aliphatic residue.

Claim 18 (cancelled)

Claim 19 (currently amended): The compound of any one of claims 1, ~~2,~~ 5, 8, 9, 13, 14, 16, or 17 wherein said compound exhibits antibacterial activity against one or more Gram-negative bacterium selected from the group consisting of *E. coli, H. influenzae, S. euteriditis, S. typhimurium, B. pertussis, Y. pestis, Y. entarocolitica, H. pylori* and *K. pneumoniae*.

Claims 20-135 (cancelled)

Claim 136 (previously presented): An isolated compound which inhibits pilus assembly, the compound consisting of SEQ ID NO: 12.

Claim 137 (previously presented): An isolated compound which inhibits pilus assembly, the compound consisting essentially of SEQ ID NO: 12, wherein the compound is a mimic of an amino terminal motif of a pilus subunit.

Claim 138 (previously presented): An isolated compound which inhibits pilus assembly, the compound comprising a mimic of an amino terminal motif of a pilus subunit, wherein the mimic comprises SEQ ID NO:12.

Claim 139 (previously presented): The compound of claim 138 wherein the compound competitively binds to a pilus subunit hydrophobic groove.

Claim 140-158 (cancelled)

Claim 159 **(new)** The compound of claim 1 wherein the compound consists essentially of a 10 to 20 residue peptide according to formula (I).

Claim 160 **(new)** The compound of claim 16 wherein the compound consists essentially of a 7 to 17 residue peptide according to formula (II).

CONCLUSION

Applicants request an entry of the specification and claim amendments and solicit allowance of all pending claims. The Office is invited to contact the undersigned attorney should any issue remain unsolved.

The Commissioner is hereby authorized to charge any underpayment and credit any overpayment of government fees to Deposit Account No. 19-1345.

Respectfully submitted,

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